

Comparative Sequencing and Analysis of Multiple Desulfovibrio and Other Sulfate Reducing Species

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As part of the work being done for the DOE GTL:Genomics program, the Virtual Institute for Microbial Stress and Survival (VIMSS) is sequencing multiple relatives of the environmental microbe *Desulfovibrio vulgaris* Hildenborough at several phylogenetic levels to aide in the analysis and annotation, as well as understanding larger questions of sulfate reduction and environmental stress response. We have sought to balance the selection of species based on the resources available for each species and the phylogenetic position the species occupies. By sequencing multiple *Desulfovibrio* species, we will be able to improve our predictions for genes, regulons, operons, regulatory elements, core genes, and environmental stress response genes. Sequenced genomes so far include: *Desulfovibrio aespoeensis*, *Desulfovibrio vulgaris* Miyazaki F, *Desulfovibrio hanfordensis*, *Desulfovibrio* sp. FW1012B, *Desulfovibrio vulgaris* DP4, *Desulfovibrio vulgaris* RCH1, *Desulfovibrio salexigens* DSM 2638, *Desulfovibrio fructosovorans*, *Desulfovibrio desulfuricans* 27774 and *Desulforudis audaxviator*. Environmental isolates, such as D. FW1012B, D. hanfordensis, DvDP4, DvRCH1 are critical for understanding the DOE field research sites. Other species such as D. aespoeensis play a role in geochemical radionuclei migration in the deep sub-surface. Here we describe our initial analysis of *Desulfovibrio* species.